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#3

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/689,730

DATE: 12/11/2001
TIME: 18:17:14

Input Set : **N:\Crf3\RULE60\09689730.raw**
Output Set: **N:\CRF3\12112001\I689730.raw**

P.5

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 1 <110> APPLICANT: SEIKI, Motoharu
 2         SATO, Hiroshi
 3         SHINAGAWA, Akira
 4 <120> TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
 5 <130> FILE REFERENCE: 55-290P
 6 <140> CURRENT APPLICATION NUMBER: 09/689,730
 7 <141> CURRENT FILING DATE: 2000-10-13
 8 <150> PRIOR APPLICATION NUMBER: US/08/448,489
 9 <151> PRIOR FILING DATE: 1995-06-07
10 <160> NUMBER OF SEQ ID NOS: 19
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ENTERED

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14 <211> LENGTH: 582
15 <212> TYPE: PRT
16 <213> ORGANISM: Homo sapiens
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20     Thr Leu Gly Thr Ala Leu Ala Ser Leu Gly Ser Ala Gln Ser Ser Ser
21                  20                  25                  30
22     Phe Ser Pro Glu Ala Trp Leu Gln Gln Tyr Gly Tyr Leu Pro Pro Gly
23              35                  40                  45
24     Asp Leu Arg Thr His Thr Gln Arg Ser Pro Gln Ser Leu Ser Ala Ala
25          50                  55                  60
26     Ile Ala Ala Met Gln Lys Phe Tyr Gly Leu Gln Val Thr Gly Lys Ala
27      65                  70                  75                  80
28     Asp Ala Asp Thr Met Lys Ala Met Arg Arg Pro Arg Cys Gly Val Pro
29                  85                  90                  95
30     Asp Lys Phe Gly Ala Glu Ile Lys Ala Asn Val Arg Arg Lys Arg Tyr
31                 100                 105                 110
32     Ala Ile Gln Gly Leu Lys Trp Gln His Asn Glu Ile Thr Phe Cys Ile
33                 115                 120                 125
34     Gln Asn Tyr Thr Pro Lys Val Gly Glu Tyr Ala Thr Tyr Glu Ala Ile
35                 130                 135                 140
36     Arg Lys Ala Phe Arg Val Trp Glu Ser Ala Thr Pro Leu Arg Phe Arg
37     145                 150                 155                 160
38     Glu Val Pro Tyr Ala Tyr Ile Arg Glu Gly His Glu Lys Gln Ala Asp
39                 165                 170                 175
40     Ile Met Ile Phe Phe Ala Glu Gly Phe His Gly Asp Ser Thr Pro Phe
41                 180                 185                 190
42     Asp Gly Glu Gly Gly Phe Leu Ala His Ala Tyr Phe Pro Gly Pro Asn
43                 195                 200                 205
44     Ile Gly Gly Asp Thr His Phe Asp Ser Ala Glu Pro Trp Thr Val Arg
45                 210                 215                 220
46     Asn Glu Asp Leu Asn Gly Asn Asp Ile Phe Leu Val Ala Val His Glu
47     225                 230                 235                 240
48     Leu Gly His Ala Leu Gly Leu Glu His Ser Ser Asp Pro Ser Ala Ile
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53                          275                   280                   285
54        Phe Pro Thr Lys Met Pro Pro Gln Pro Arg Thr Thr Ser Arg Pro Ser
55                          290                   295                   300
56        Val Pro Asp Lys Pro Lys Asn Pro Thr Tyr Gly Pro Asn Ile Cys Asp
57        305                   310                   315                   320
58        Gly Asn Phe Asp Thr Val Ala Met Leu Arg Gly Glu Met Phe Val Phe
59                          325                   330                   335
60        Lys Lys Arg Trp Phe Trp Arg Val Arg Asn Asn Gln Val Met Asp Gly
61                          340                   345                   350
62        Tyr Pro Met Pro Ile Gly Gln Phe Trp Arg Gly Leu Pro Ala Ser Ile
63                          355                   360                   365
64        Asn Thr Ala Tyr Glu Arg Lys Asp Gly Lys Phe Val Phe Phe Lys Gly
65        370                   375                   380
66        Asp Lys His Trp Val Phe Asp Glu Ala Ser Leu Glu Pro Gly Tyr Pro
67        385                   390                   395                   400
68        Lys His Ile Lys Glu Leu Gly Arg Gly Leu Pro Thr Asp Lys Ile Asp
69                          405                   410                   415
70        Ala Ala Leu Phe Trp Met Pro Asn Gly Lys Thr Tyr Phe Phe Arg Gly
71                          420                   425                   430
72        Asn Lys Tyr Tyr Arg Phe Asn Glu Glu Leu Arg Ala Val Asp Ser Glu
73                          435                   440                   445
74        Tyr Pro Lys Asn Ile Lys Val Trp Glu Gly Ile Pro Glu Ser Pro Arg
75        450                   455                   460
76        Gly Ser Phe Met Gly Ser Asp Glu Val Phe Thr Tyr Phe Tyr Lys Gly
77        465                   470                   475                   480
78        Asn Lys Tyr Trp Lys Phe Asn Asn Gln Lys Leu Lys Val Glu Pro Gly
79                          485                   490                   495
80        Tyr Pro Lys Ser Ala Leu Arg Asp Trp Met Gly Cys Pro Ser Gly Gly
81                          500                   505                   510
82        Arg Pro Asp Glu Gly Thr Glu Glu Glu Thr Glu Val Ile Ile Ile Glu
83                          515                   520                   525
84        Val Asp Glu Glu Gly Gly Gly Ala Val Ser Ala Ala Ala Val Val Leu
85                          530                   535                   540
86        Pro Val Leu Leu Leu Leu Leu Val Leu Ala Val Gly Leu Ala Val Phe
87        545                   550                   555                   560
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91                          580
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94 <211> LENGTH: 3403
95 <212> TYPE: DNA
96 <213> ORGANISM: Homo sapiens
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100         gccccaagac cctcccgttg tctcctgctc cccctgctca cgctcggcac cgcgctcgcc 180
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103         gccatcgctg ccatgcagaa gttttacggc ttgcaagtaa caggcaaagc tgatgcagac 360
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105         aaggccaatg ttcgaaggaa gcgctacgcc atccagggtc tcaaatggca acataatgaa 480
106         attactttct gcatccagaa ttacacccccc aaggtgggcg agtatgccac atacgaggcc 540
107         attcgcaagg cgttccgcgt gtgggagagt gccacaccac tgcgcttccg cgaggtgccc 600
108         tatgcctaca tccgtgaggg ccatgagaag caggccgaca tcatgatctt ctttgccgag 660
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110         ttcccagggc ccaacattgg aggagacacc cactttgact ctgccgagcc ttggactgtc 780
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118         ctgcctgcgt ccatcaacac tgcctacgag aggaaggatg gcaaattcgt cttcttcaaa 1260
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122         gcagtggata gcgagtaccc caagaacatc aaagtctggg aagggatccc tgagtctccc 1500
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150      ttccctggtg ccagcacccc tcaagcctgt ctcaccagtg gcctgccctc tcgctccccc 3180
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160 <220> FEATURE:
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163 <400> SEQUENCE: 3
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168 <211> LENGTH: 9
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170 <213> ORGANISM: Unknown
171 <220> FEATURE:
172 <223> OTHER INFORMATION: Description of Unknown Organism: Highly conserved
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176          1               5
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179 <211> LENGTH: 20
180 <212> TYPE: DNA
181 <213> ORGANISM: Artificial Sequence
182 <220> FEATURE:
183 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
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188 <211> LENGTH: 25
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190 <213> ORGANISM: Artificial Sequence
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192 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
193 <400> SEQUENCE: 6
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198 <212> TYPE: PRT
199 <213> ORGANISM: Homo sapiens
200 <400> SEQUENCE: 7
201      Gly Gly Gly Ala Val Ser Ala Ala Ala Val Val Leu Pro Val Leu Leu
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Input Set : N:\Crf3\RULE60\09689730.raw

Output Set: N:\CRF3\12112001\I689730.raw

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208 <212> TYPE: PRT
209 <213> ORGANISM: Homo sapiens
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212              1              5                      10
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215 <211> LENGTH: 14
216 <212> TYPE: PRT
217 <213> ORGANISM: Homo sapiens
218 <400> SEQUENCE: 9
219          Asp Gly Asn Phe Asp Thr Val Ala Met Leu Arg Gly Glu Met
220              1              5                      10
222 <210> SEQ ID NO: 10
223 <211> LENGTH: 15
224 <212> TYPE: PRT
225 <213> ORGANISM: Homo sapiens
226 <400> SEQUENCE: 10
227          Pro Lys Ser Ala Leu Arg Asp Trp Met Gly Cys Pro Ser Gly Gly
228              1              5                      10                    15
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231 <211> LENGTH: 489
232 <212> TYPE: PRT
233 <213> ORGANISM: Unknown
234 <220> FEATURE:
235 <223> OTHER INFORMATION: X = UNKNOWN
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237 <223> OTHER INFORMATION: Description of Unknown Organism: Known Member of
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243                      20                      25                    30
244          Ala Leu Pro Pro Asp Val His His Leu His Ala Glu Arg Arg Gly Pro
245                      35                      40                    45
246          Gln Pro Trp His Ala Ala Leu Pro Ser Ser Pro Ala Pro Ala Pro Ala
247                      50                      55                    60
248          Thr Gln Glu Ala Pro Arg Pro Ala Ser Ser Leu Arg Pro Pro Arg Cys
249                      65                      70                    75                    80
250          Gly Val Pro Asp Pro Ser Asp Gly Leu Ser Ala Arg Asn Arg Gln Lys
251                      85                      90                    95
252          Arg Phe Val Leu Ser Gly Gly Arg Trp Glu Lys Thr Asp Leu Thr Tyr
253                      100                     105                   110
254          Arg Ile Leu Arg Phe Pro Trp Gln Leu Val Gln Glu Gln Val Arg Gln
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VERIFICATION SUMMARY
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Input Set : **N:\Crf3\RULE60\09689730.raw**
Output Set: **N:\CRF3\12112001\I689730.raw**

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L:300 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:440 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:440 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:440 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:679 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:16
L:679 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
L:679 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
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